IN THE SPECIFICATION:

Please replace the 1st paragraph (lines 1-2) on page 2 with the following paragraph:

transporter nomenclature supplement. Trends Pharmacol. Sci., Elsevier, pp. 65-68 (1997) [and http://www-biology.ucsd.edu/~msaier/transport/titlepage2.html].

Please replace the 1st paragraph (lines 1-11) on page 21 with the following paragraph:

into the GAP program in the GCG software package ~~(available at http://www.gcg.com)~~, using either a Blossom 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (Devereux, J., *et al., Nucleic Acids Res. 12(1)*:387 (1984)) ~~(available at http://www.gcg.com)~~, using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. In another embodiment, the percent identity between two amino acid or nucleotide sequences is determined using the algorithm of E. Myers and W. Miller (CABIOS, 4:11-17 (1989)) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4.